BLAST ® » blastn suite » RID-ZZN3UUXD015

BLAST Results

Questions/comments

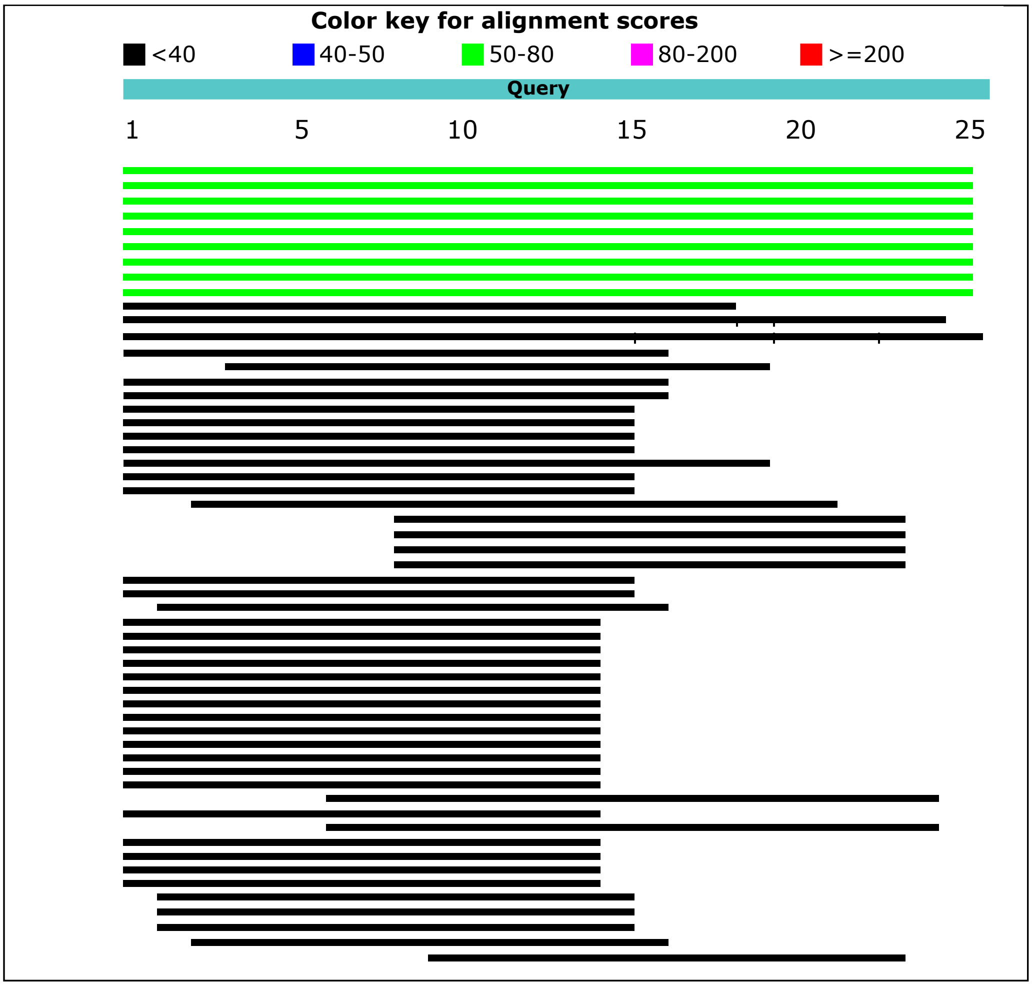
Job title: Nucleotide Sequence (25 letters)

RID ZZN3UUXD015 (Expires on 11-30 18:58 pm)
Query ID lcl|Query_109169
Description None
Molecule type nucleic acid
Query Length 25

Database Name Human G+T (2 databases)
Description
Program BLASTN 2.8.1+

Graphic Summary

Distribution of the top 197 Blast Hits on 97 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Transcripts						
Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 8, mRNA	50.1	50.1	100%	2e-05	100%	NM_001291157.1
Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 2, mRNA	50.1	50.1	100%	2e-05	100%	NM_198241.2
Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 7, mRNA	50.1	50.1	100%	2e-05	100%	NM_001194947.1
Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 6, mRNA	50.1	50.1	100%	2e-05	100%	NM_001194946.1
Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 3, mRNA	50.1	50.1	100%	2e-05	100%	NM_198244.2
Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 4, mRNA	50.1	50.1	100%	2e-05	100%	NM_198242.2
Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 5, mRNA	50.1	50.1	100%	2e-05	100%	NM_004953.4
Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 1, mRNA	50.1	50.1	100%	2e-05	100%	NM_182917.4
Homo sapiens fibroblast growth factor 23 (FGF23), mRNA	36.2	36.2	72%	0.34	100%	NM_020638.2
PREDICTED: Homo sapiens cyclin dependent kinase 13 (CDK13), transcript variant X2, mRNA	30.2	30.2	60%	21	100%	XM_017012751.2
PREDICTED: Homo sapiens cyclin dependent kinase 13 (CDK13), transcript variant X1, mRNA	30.2	30.2	60%	21	100%	XM_017012750.2
Homo sapiens cyclin dependent kinase 13 (CDK13), transcript variant 2, mRNA	30.2	30.2	60%	21	100%	NM_031267.3
Homo sapiens cyclin dependent kinase 13 (CDK13), transcript variant 1, mRNA	30.2	30.2	60%	21	100%	NM_003718.4
PREDICTED: Homo sapiens ubiquitin like modifier activating enzyme 3 (UBA3), transcript variant X2, mRNA	30.2	30.2	60%	21	100%	XM_011534211.1
PREDICTED: Homo sapiens ubiquitin like modifier activating enzyme 3 (UBA3), transcript variant X1, mRNA	30.2	30.2	60%	21	100%	XM_011534210.1
Homo sapiens ubiquitin like modifier activating enzyme 3 (UBA3), transcript variant 2, mRNA	30.2	30.2	60%	21	100%	NM_198195.1
Homo sapiens ubiquitin like modifier activating enzyme 3 (UBA3), transcript variant 1, mRNA	30.2	30.2	60%	21	100%	NM_003968.3
PREDICTED: Homo sapiens zinc finger protein 273 (ZNF273), transcript variant X7, mRNA	28.2	28.2	56%	84	100%	XM_024446641.1
PREDICTED: Homo sapiens zinc finger protein 273 (ZNF273), transcript variant X6, mRNA	28.2	28.2	56%	84	100%	XM_024446640.1
PREDICTED: Homo sapiens zinc finger protein 273 (ZNF273), transcript variant X5, mRNA	28.2	28.2	56%	84	100%	XM_024446639.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens zinc finger protein 273 (ZNF273), transcript variant X4, mRNA	28.2	28.2	56%	84	100%	XM_024446638.1
PREDICTED: Homo sapiens zinc finger protein 273 (ZNF273), transcript variant X3, mRNA	28.2	28.2	56%	84	100%	XM_024446637.1
PREDICTED: Homo sapiens zinc finger protein 273 (ZNF273), transcript variant X2, mRNA	28.2	28.2	56%	84	100%	XM_024446636.1
PREDICTED: Homo sapiens zinc finger protein 273 (ZNF273), transcript variant X1, mRNA	28.2	28.2	56%	84	100%	XM_024446635.1
PREDICTED: Homo sapiens adhesion G protein-coupled receptor B3 (ADGRB3), transcript variant X8, mRNA	28.2	28.2	56%	84	100%	XM_011536011.3
PREDICTED: Homo sapiens adhesion G protein-coupled receptor B3 (ADGRB3), transcript variant X7, mRNA	28.2	28.2	56%	84	100%	XM_024446503.1
PREDICTED: Homo sapiens adhesion G protein-coupled receptor B3 (ADGRB3), transcript variant X6, mRNA	28.2	28.2	56%	84	100%	XM_024446502.1
PREDICTED: Homo sapiens adhesion G protein-coupled receptor B3 (ADGRB3), transcript variant X5, mRNA	28.2	28.2	56%	84	100%	XM_024446501.1
PREDICTED: Homo sapiens adhesion G protein-coupled receptor B3 (ADGRB3), transcript variant X1, mRNA	28.2	28.2	56%	84	100%	XM_005248752.3
PREDICTED: Homo sapiens uncharacterized LOC112268421 (LOC112268421), ncRNA	28.2	28.2	56%	84	100%	XR_002959410.1
PREDICTED: Homo sapiens uncharacterized LOC105378536 (LOC105378536), transcript variant X4, ncRNA	28.2	28.2	72%	84	94%	XR_953252.2
PREDICTED: Homo sapiens adhesion G protein-coupled receptor B3 (ADGRB3), transcript variant X4, mRNA	28.2	28.2	56%	84	100%	XM_011536009.2
PREDICTED: Homo sapiens uncharacterized LOC105378536 (LOC105378536), transcript variant X4, ncRNA	28.2	28.2	72%	84	94%	XR_946428.2
Homo sapiens adhesion G protein-coupled receptor B3 (ADGRB3), mRNA	28.2	28.2	56%	84	100%	NM_001704.2
Homo sapiens zinc finger protein 273 (ZNF273), transcript variant 1, mRNA	28.2	28.2	56%	84	100%	NM_021148.2
Homo sapiens zinc finger protein 273 (ZNF273), transcript variant 2, non-coding RNA	28.2	28.2	56%	84	100%	NR_003099.1
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X15, mRNA	28.2	28.2	56%	84	100%	XM_024446349.1
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X13, misc_RNA	28.2	28.2	56%	84	100%	XR_001743217.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X12, misc_RNA	28.2	28.2	56%	84	100%	XR_001743216.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X11, misc_RNA	28.2	28.2	56%	84	100%	XR_001743215.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X10, mRNA	28.2	28.2	56%	84	100%	XM_011535528.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X9, mRNA	28.2	28.2	56%	84	100%	XM_017010356.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X8, mRNA	28.2	28.2	56%	84	100%	XM_011535527.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X7, mRNA	28.2	28.2	56%	84	100%	XM_011535525.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X6, mRNA	28.2	28.2	56%	84	100%	XM_017010353.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X5, misc_RNA	28.2	28.2	56%	84	100%	XR_001743213.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X2, mRNA	28.2	28.2	56%	84	100%	XM_017010350.2
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X1, mRNA	28.2	28.2	56%	84	100%	XM_011535524.2
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 20, mRNA	28.2	28.2	56%	84	100%	NM_001350313.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 18, mRNA	28.2	28.2	56%	84	100%	NM_001350311.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 13, mRNA	28.2	28.2	56%	84	100%	NM_001350306.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 17, mRNA	28.2	28.2	56%	84	100%	NM_001350310.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 10, mRNA	28.2	28.2	56%	84	100%	NM_001350303.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 12, mRNA	28.2	28.2	56%	84	100%	NM_001350305.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 15, mRNA	28.2	28.2	56%	84	100%	NM_001350308.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 19, mRNA	28.2	28.2	56%	84	100%	NM_001350312.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 14, mRNA	28.2	28.2	56%	84	100%	NM_001350307.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 22, mRNA	28.2	28.2	56%	84	100%	NM_001350315.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 8, mRNA	28.2	28.2	56%	84	100%	NM_001350301.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 21, mRNA	28.2	28.2	56%	84	100%	NM_001350314.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 11, mRNA	28.2	28.2	56%	84	100%	NM_001350304.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 7, mRNA	28.2	28.2	56%	84	100%	NM_001350299.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 9, mRNA	28.2	28.2	56%	84	100%	NM_001350302.1
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 16, mRNA	28.2	28.2	56%	84	100%	NM_001350309.1
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X4, mRNA	28.2	28.2	56%	84	100%	XM_017010352.1
PREDICTED: Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant X3, mRNA	28.2	28.2	56%	84	100%	XM_017010351.1
PREDICTED: Homo sapiens uncharacterized LOC107986059 (LOC107986059), ncRNA	28.2	28.2	56%	84	100%	XR_001740585.1
PREDICTED: Homo sapiens transcriptional adaptor 2A (TADA2A), transcript variant X8, mRNA	28.2	28.2	56%	84	100%	XM_017024985.1
PREDICTED: Homo sapiens transcriptional adaptor 2A (TADA2A), transcript variant X6, mRNA	28.2	28.2	56%	84	100%	XM_017024983.1
PREDICTED: Homo sapiens transcriptional adaptor 2A (TADA2A), transcript variant X5, mRNA	28.2	28.2	56%	84	100%	XM_006722044.3
Homo sapiens erythrocyte membrane protein band 4.1 like 2 (EPB41L2), transcript variant 6, mRNA	28.2	28.2	56%	84	100%	NM_001252660.1
Genomic sequences[show first]						
Homo sapiens chromosome 3, GRCh38.p12 Primary Assembly	50.1	1289	100%	2e-05	100%	NC_000003.12
Homo sapiens chromosome 12, GRCh38.p12 Primary Assembly	36.2	696	96%	0.34	100%	NC_000012.12
Homo sapiens chromosome 2, GRCh38.p12 Primary Assembly	32.2	1928	100%	5.4	100%	NC_000002.12
Homo sapiens chromosome 4, GRCh38.p12 Primary Assembly	32.2	1490	100%	5.4	100%	NC_000004.12
Homo sapiens chromosome 10, GRCh38.p12 Primary Assembly	32.2	1068	100%	5.4	100%	NC_000010.11
Homo sapiens chromosome 13, GRCh38.p12 Primary Assembly	32.2	434	100%	5.4	100%	NC_000013.11
Homo sapiens chromosome 6, GRCh38.p12 Primary Assembly	32.2	943	100%	5.4	100%	NC_000006.12
Homo sapiens chromosome 5, GRCh38.p12 Primary Assembly	30.2	795	92%	21	95%	NC_000005.10
Homo sapiens chromosome 7, GRCh38.p12 Primary Assembly	30.2	787	100%	21	100%	NC_000007.14
Homo sapiens chromosome 8, GRCh38.p12 Primary Assembly	30.2	803	96%	21	100%	NC_000008.11

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 9, GRCh38.p12 Primary Assembly	30.2	832	100%	21	95%	NC_000009.12
Homo sapiens chromosome 18, GRCh38.p12 Primary Assembly	30.2	480	96%	21	100%	NC_000018.10
Homo sapiens chromosome 20, GRCh38.p12 Primary Assembly	30.2	381	92%	21	100%	NC_000020.11
Homo sapiens chromosome X, GRCh38.p12 Primary Assembly	30.2	1038	88%	21	100%	NC_000023.11
Homo sapiens chromosome 1, GRCh38.p12 Primary Assembly	28.2	878	92%	84	100%	NC_000001.11
Homo sapiens chromosome 14, GRCh38.p12 Primary Assembly	28.2	369	100%	84	100%	NC_000014.9
Homo sapiens chromosome 16, GRCh38.p12 Primary Assembly	28.2	668	92%	84	100%	NC_000016.10
Homo sapiens chromosome 17, GRCh38.p12 Primary Assembly	28.2	403	88%	84	100%	NC_000017.11
Homo sapiens chromosome 19, GRCh38.p12 Primary Assembly	28.2	161	64%	84	100%	NC_000019.10
Homo sapiens chromosome 21, GRCh38.p12 Primary Assembly	28.2	240	92%	84	100%	NC_000021.9
Homo sapiens chromosome 11, GRCh38.p12 Primary Assembly	28.2	634	88%	84	100%	NC_000011.10
Homo sapiens chromosome 15, GRCh38.p12 Primary Assembly	28.2	264	92%	84	100%	NC_000015.10
Homo sapiens chromosome 17 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_1 HSCHR17_7_CTG4	28.2	28.2	56%	84	100%	NT_187614.1
Homo sapiens chromosome 16 unlocalized genomic scaffold, GRCh38.p12 Primary Assembly HSCHR16_RANDOM_CTG1	28.2	28.2	56%	84	100%	NT_187383.1
Homo sapiens chromosome 22, GRCh38.p12 Primary Assembly	26.3	183	68%	332	100%	NC_000022.11
Homo sapiens chromosome Y, GRCh38.p12 Primary Assembly	26.3	26.3	52%	332	100%	NC_000024.10

Alignments

Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 8, mRNA
Sequence ID: **NM_001291157.1** Length: 5581 Number of Matches: 1
Range 1: 2845 to 2869

Score	Expect	Identities	Gaps	Strand	Frame
50.1 bits(25)	2e-05()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1     AAGCTGTTGTTGAATCGATGTCAGA  25
             |||||||||||||||||||||||||
Sbjct  2845  AAGCTGTTGTTGAATCGATGTCAGA  2869
```

Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 2, mRNA
Sequence ID: **NM_198241.2** Length: 5538 Number of Matches: 1
Range 1: 2792 to 2816

Score	Expect	Identities	Gaps	Strand	Frame
50.1 bits(25)	2e-05()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1     AAGCTGTTGTTGAATCGATGTCAGA  25
             |||||||||||||||||||||||||
Sbjct  2792  AAGCTGTTGTTGAATCGATGTCAGA  2816
```

Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 7, mRNA
Sequence ID: **NM_001194947.1** Length: 5502 Number of Matches: 1
Range 1: 2756 to 2780

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
50.1 bits(25)	2e-05()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1     AAGCTGTTGTTGAATCGATGTCAGA  25
             |||||||||||||||||||||||||
Sbjct  2756  AAGCTGTTGTTGAATCGATGTCAGA  2780
```

Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 6, mRNA
Sequence ID: **NM_001194946.1** Length: 5559 Number of Matches: 1
Range 1: 2813 to 2837

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
50.1 bits(25)	2e-05()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1     AAGCTGTTGTTGAATCGATGTCAGA  25
             |||||||||||||||||||||||||
Sbjct  2813  AAGCTGTTGTTGAATCGATGTCAGA  2837
```

Homo sapiens eukaryotic translation initiation factor 4 gamma 1 (EIF4G1), transcript variant 3, mRNA
Sequence ID: **NM_198244.2** Length: 5300 Number of Matches: 1
Range 1: 2554 to 2578

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
50.1 bits(25)	2e-05()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1     AAGCTGTTGTTGAATCGATGTCAGA  25
             |||||||||||||||||||||||||
Sbjct  2554  AAGCTGTTGTTGAATCGATGTCAGA  2578
```